

1 MMQKLQMYVVY 10	11 IYLFMLIAAG 20	21 PV-----DLNEGSER 30 Mouse
1 M I QKPQMYVVY 10	11 IYLFVLI AAG 20	21 PV-----DLNEDSER 30 Rat
1 -M QKLQ L CVY 9	10 IYLFMLI VAG 19	20 PV-----DLNENSEQ 29 Human
1 -M QKLQ L CVY 9	10 IYLFMLI VAG 19	20 PV-----DLNENSEQ 29 Baboon
1 -M QKLQ I SVY 9	10 IYLFMLI VAG 19	20 PV-----DLNENSEQ 29 Bovine
1 -M QKLQ I YVY 9	10 IYLFMLI VAG 19	20 PV-----DLNENSEQ 29 Porcine
1 -M QKLQ I FVY 9	10 IYLFMLLVAG 19	20 PV-----DLNENSEQ 29 Ovine
1 -M QKLA VVVY 9	10 IYLFMQI AVD 19	20 PV-----ALDGSSQP 29 Chicken
1 -M Q I LA VVYV 9	10 IYLFMQI LVH 19	20 PV-----ALDGSSQP 29 Turkey
1 -MH FTQ-----VL 7	8 ISLS VL I ACG 17	18 PVGYGDITAHQQP 30 Zebrafish
31 EENVEKEGLC 40	41 NACA WRQNTR 50	51 YS RIE AIKIQ 60 Mouse
31 EANVEKEGLC 40	41 NACA WRQNTR 50	51 YS RIE AIKIQ 60 Rat
30 KENVEKEGLC 39	40 NACT WRQNTK 49	50 SS RIE AIKIQ 59 Human
30 KENVEKEGLC 39	40 NACT WRQNTK 49	50 SS RIE AIKIQ 59 Baboon
30 KENVEKEGLC 39	40 NACL WRE NTT 49	50 SS RLE AIKIQ 59 Bovine
30 KENVEKEGLC 39	40 NACMWRQNTK 49	50 SS RLE AIKIQ 59 Porcine
30 KENVEKKGLC 39	40 NACL WRQNNK 49	50 SS RLE AIKIQ 59 Ovine
30 TENAEKDGLC 39	40 NACT WRQNTK 49	50 SS RIE AIKIQ 59 Chicken
30 TENAEKDGLC 39	40 NACT WRQNTK 49	50 SS RIE AIKIQ 59 Turkey
31 STAT EES ELC 40	41 S TCE FRQHSK 50	51 LM RLHAIKSQ 60 Zebrafish
61 ILSKLRLETA 70	71 PNISKDA IRQ 80	81 LLPRAPPLRE 90 Mouse
61 ILSKLRLETA 70	71 PNISKDA IRQ 80	81 LLPRAPPLRE 90 Rat
60 ILSKLRLETA 69	70 PNISKDV IRQ 79	80 LLPKAPPLRE 89 Human
60 ILSKLRLETA 69	70 PNISKDA IRQ 79	80 LLPKAPPLRE 89 Baboon
60 ILSKLRLETA 69	70 PNISKDA IRQ 79	80 LLPRAPPLRE 89 Bovine
60 ILSKLRLETA 69	70 PNISKDA IRQ 79	80 LLPRAPPLRE 89 Porcine
60 ILSKLRLETA 69	70 PNISKDA IRQ 79	80 LLPRAPPLRE 89 Ovine
60 ILSKLRLEQA 69	70 PNISRDV IKQ 79	80 LLPRAPPLQE 89 Chicken
60 ILSKLRLEQA 69	70 PNISRDV IKQ 79	80 LLPRAPPLQE 89 Turkey
61 ILSKLRLKQA 70	71 PNISRDVVKQ 80	81 LLPRAPPLQQ 90 Zebrafish
91 LI DQYDVQRD 100	101 DS SDGSLEDD 110	111 DYH ATTET II 120 Mouse
91 LI DQYDVQRD 100	101 DS SDGSLEDD 110	111 DYH ATTET II 120 Rat
90 LI DQYDVQRD 99	100 DS SDGSLEDD 109	110 DYH ATTET II 119 Human
90 LI DQYDVQRD 99	100 DS SDGSLEDD 109	110 DYH ATTET II 119 Baboon
90 LI DQFDVQRD 99	100 AS SDGSLEDD 109	110 DYH ARTETV I 119 Bovine
90 LI DQYDVQRD 99	100 DS SDGSLEDD 109	110 DYH ATTET II 119 Porcine
90 LI DQYDVQRD 99	100 DS SDGSLEDD 109	110 DYH VTTETV I 119 Ovine
90 LI DQYDVQRD 99	100 DS SDGSLEDD 109	110 DYH ATTET II 119 Chicken
90 LI DQYDVQRD 99	100 DS SDGSLEDD 109	110 DYH ATTET II 119 Turkey
91 LLDQYDVLGD 100	101 DSKDGAVEED 110	111 DEH ATTET IM 120 Zebrafish

FIG. 1A

121 TMPTESDFLM 130	131 QADGKPCCF 140	141 FKFSSSKIQYN 150 Mouse
121 TMPTESDFLM 130	131 QADGKPCCF 140	141 FKFSSSKIQYN 150 Rat
120 TMPTESDFLM 129	130 QVDGKPCCF 139	140 FKFSSSKIQYN 149 Human
120 TMPTESDFLM 129	130 QVDGKPCCF 139	140 FKFSSSKIQYN 149 Baboon
120 TMPTESDLL T 129	130 QVEGKPCCF 139	140 FKFSSSKIQYN 149 Bovine
120 TMPTESDLL M 129	130 QVEGKPCCF 139	140 FKFSSSKIQYN 149 Porcine
120 TMPTESDLL A 129	130 EVQEKPCCF 139	140 FKFSSSKIQHN 149 Ovine
120 TMPTESDFL V 129	130 QMEGKPCCF 139	140 FKFSSSKIQYN 149 Chicken
120 TMPTESDFL V 129	130 QMEGKPCCF 139	140 FKFSSSKIQYN 149 Turkey
121 TMATEPDPI V 130	131 QVDRKPCCF 140	141 FS FSPKIQAN 150 Zebrafish
151 KVVKAQLW IY 160	161 LRP VKTPPTV 170	171 FVQILRLIKP 180 Mouse
151 KVVKAQLW IY 160	161 LRAVKTPPTV 170	171 FVQILRLIKP 180 Rat
150 KVVKAQLW IY 159	160 LRP VETPTTV 169	170 FVQILRLIKP 179 Human
150 KVVKAQLW IY 159	160 LRP VETPTTV 169	170 FVQILRLIKP 179 Baboon
150 KLVKAQLW IY 159	160 LRP VKTPATV 169	170 FVQILRLIKP 179 Bovine
150 KVVKAQLW IY 159	160 LRP VKTPPTV 169	170 FVQILRLIKP 179 Porcine
150 KVVKAQLW IY 159	160 LRP VKTPPTV 169	170 FVQILRLIKP 179 Ovine
150 KVVKAQLW IY 159	160 LRQVQKPTTV 169	170 FVQILRLIKP 179 Chicken
150 KVVKAQLW IY 159	160 LRQVQKPTTV 169	170 FVQILRLIKP 179 Turkey
151 R I VRAQLWVH 160	161 LRP AEEATTV 169	170 FLQISRLM-P 179 Zebrafish
181 MKDGTRYTGI 190	191 RSLKLDMSPG 200	201 TGIWQSIDVK 210 Mouse
181 MKDGTRYTGI 190	191 RSLKLDMSPG 200	201 TGIWQSIDVK 210 Rat
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Human
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Baboon
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Bovine
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Porcine
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Ovine
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Chicken
180 MKDGTRYTGI 189	190 RSLKLDMNPG 199	200 TGIWQSIDVK 209 Turkey
180 V KDGGRHR-I 188	189 RSLK IDV NAG 198	199 VTSWQSIDVK 208 Zebrafish
211 TVLQNWLKQP 220	221 ESNLGIEIKA 230	231 LD ENGHDLAV 240 Mouse
211 TVLQNWLKQP 220	221 ESNLGIEIKA 230	231 LD ENGHDLAV 240 Rat
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Human
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Baboon
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Bovine
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Porcine
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 LD ENGHDLAV 239 Ovine
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 FD ETGRDLAV 239 Chicken
210 TVLQNWLKQP 219	220 ESNLGIEIKA 229	230 FD ENGRDLAV 239 Turkey
209 QVLTVWLKQP 218	219 ETNRGIEINA 228	229 YDAKGNDLAV 238 Zebrafish

FIG. 1B

241 TFPGPGEGL 250	251 NPFLEVKTVD 260	261 TPKRSRRDFG 270 Mouse
241 TFPGPGEGL 250	251 NPFLEVKTVD 260	261 TPKRSRRDFG 270 Rat
240 TFPGPGEGL 249	250 NPFLEVKTVD 259	260 TPKRSRRDFG 269 Human
240 TFPGPGEGL 249	250 NPFLEVKTVD 259	260 TPKRSRRDFG 269 Baboon
240 TFPEPGEDGL 249	250 TPFLEVKTVD 259	260 TPKRSRRDFG 269 Bovine
240 TFPGPGEGL 249	250 NPFLEVKTVD 259	260 TPKRSRRDFG 269 Porcine
240 TFPEPGEEGL 249	250 NPFLEVKTVD 259	260 TPKRSRRDFG 269 Ovine
240 TFPGPGEGL 249	250 NPFLEVRVTD 259	260 TPKRSRRDFG 269 Chicken
240 TFPGPGEGL 249	250 NPFLEVRVTD 259	260 TPKRSRRDFG 269 Turkey
239 TSTETGEDGL 248	249 LPFMEVKI SE 258	259 GPKRIRRDSG 268 Zebrafish
271 LDCDEHSTES 280	281 RCCRYPLTVD 290	291 FEAFGWDWII 300 Mouse
271 LDCDEHSTES 280	281 RCCRYPLTVD 290	291 FEAFGWDWII 300 Rat
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEAFGWDWII 299 Human
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEALGWDWII 299 Baboon
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEAFGWDWII 299 Bovine
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEAFGWDWII 299 Porcine
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEAFGWDWII 299 Ovine
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEAFGWDWII 299 Chicken
270 LDCDEHSTES 279	280 RCCRYPLTVD 289	290 FEAFGWDWII 299 Turkey
269 LDCDENSSES 278	279 RCCRYPLTVD 288	289 FEDFGWDWII 298 Zebrafish
301 APKRYKANYC 310	311 SGECE FV FLQ 320	321 KYPHTHLVHQ 330 Mouse
301 APKRYKANYC 310	311 SGECE FV FLQ 320	321 KYPHTHLVHQ 330 Rat
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Human
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Baboon
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Bovine
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Porcine
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Ovine
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Chicken
300 APKRYKANYC 309	310 SGECE FV FLQ 319	320 KYPHTHLVHQ 329 Turkey
299 APKRYKANYC 308	309 SGECDYMYLQ 318	319 KYPHTHLVNK 328 Zebrafish
331 ANPRGSAGPC 340	341 CTPTKMSPIN 350	351 MLYFNGKEQI 360 Mouse
331 ANPRGSAGPC 340	341 CTPTKMSPIN 350	351 MLYFNGKEQI 360 Rat
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Human
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Baboon
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGEGQI 359 Bovine
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Porcine
330 ANPKGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Ovine
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Chicken
330 ANPRGSAGPC 339	340 CTPTKMSPIN 349	350 MLYFNGKEQI 359 Turkey
329 ASPRGTAGPC 338	339 CTPTKMSPIN 248	349 MLYFNGKEQI 359 Zebrafish

FIG. 1C

361 IYGKIPAMVV 370 371 DRCGCS 376 Mouse
361 IYGKIPAMVV 370 371 DRCGCS 376 Rat
360 IYGKIPAMVV 369 370 DRCGCS 375 Human
360 IYGKIPAMVV 369 370 DRCGCS 375 Baboon
360 IYGKIPAMVV 369 370 DRCGCS 375 Bovine
360 IYGKIPAMVV 369 370 DRCGCS 375 Porcine
360 IYGKIPGMVV 369 370 DRCGCS 375 Ovine
360 IYGKIPAMVV 369 370 DRCGCS 375 Chicken
360 IYGKIPAMVV 369 370 DRCGCS 375 Turkey
359 IYGKIP SMVV 368 369 DRCGCS 374 Zebrafish

FIG. 1D

10 20 30 40
GGA TCC CGT TCT CGT CGC GAC TTT GGT CTG GAC TGC GAC GAA CAT
Gly Ser Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His

50 60
TCT ACC GAA AGA TCT
Ser Thr Glu Arg Ser

FIG. 2

10 20 30 40
GGA TCC TCT CGT TGC TGT CGC TAT CCG CTG ACC GTT GAC TTC GAA
Gly Ser Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu

50
AGA TCT
Arg Ser

FIG. 3

10 20 30 40
GGA TCC TTC GAA GCT TTT GGT TGG GAC TGG ATC ATT GCA CCG AAA
Gly Ser Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys

50
CGT TAT AGA TCT
Arg Tyr Arg Ser

FIG. 4

10 20 30 40
 GGA TCC AAA CGT TAT AAA GCT AAC TAT TGC TCT GGT GAA TGC GAA
 Gly Ser Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
 50
 TTC AGA TCT
 Phe Arg Ser

FIG. 5

10 20 30 40
 GGA TCC GAA TTC GTT TTC CTG CAG AAA TAT CCG CAT ACC CAT CTG
 Gly Ser Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu
 50 60 70
 GTT CAT CAG GCT AAC CCG CGT AGA TCT
 Val His Gln Ala Asn Pro Arg Arg Ser

FIG. 6

10 20 30 40
 GGA TCC GCT GGT CCG TGC TGT TAT CCG ACC AAA ATG TCT CCG ATC
 Gly Ser Ala Gly Pro Cys Cys Tyr Pro Thr Lys MET Ser Pro Ile
 50 60 70 80
 AAC ATG CTG TAT TTC AAC GGT GAA TGC CAG AGA TCT
 Asn MET Leu Tyr Phe Asn Gly Glu Cys Gln Arg Ser

FIG. 7

10 20 30 40
 GGA TCC GAA TGC CAG ATC ATT TAT TGC AAA ATC CCG GCT ATG GTT
 Gly Ser Glu Cys Gln Ile Ile Tyr Cys Lys Ile Pro Ala MET Val
 50 60 70
 GTA GAC CGT TGC GGT TGT TCT AGA TCT
 Val Asp Arg Cys Gly Cys Ser Arg Ser

FIG. 8

10 20 30 40
 GGA TCC GAA CAG AAA GAA AAC GTT GAA AAA GAA GGT CTG TGC AAC
 Gly Ser Glu Gln Lys Glu Asn Val Glu Lys Glu Gly Leu Cys Asn
 50 60
 GCT TGC CTG TGG AGA TCT
 Ala Cys Leu Trp Arg Ser

FIG. 9

10 20 30 40
 GGA TCC CAT GAC CTG GCT GTT ACC TTC CCG GAA CCG GGT GAA GAC
 Gly Ser His Asp Leu Ala Val Thr Phe Pro Glu Pro Gly Glu Asp
 50 60
 GGT CTG ACC AGA TCT
 Gly Leu Thr Arg Ser

FIG. 10

10 20 30 40
 GGA TCC ACC CCG TTC CTG GAA GTT AAA GTT ACC GAC ACT CCG AAA
 Gly Ser Thr Pro Phe Leu Glu Val Lys Val Thr Asp Thr Pro Lys

 50 60
 CGT TCT CGT AGA TCT
 Arg Ser Arg Arg Ser

FIG. 11

Entire Myostatin Protein 376

264 Myostatin Active Region 376

15 _____
17 _____ 1 _____ 13 _____
19 _____ 3 _____
5 _____ 9 _____
7 _____

FIG. 12

10 20 30 40
 GGA TCC CGT TCT CGT CGC GAC TTT GGT CTG GAC TGC GAC GAA CAT
 Gly Ser Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His

 50 60 70 80 90
 TCT ACC GAA AGA TCC TCT CGT TGC TGT CGC TAT CCG CTG ACC GTT
 Ser Thr Glu Arg Ser Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val

 100 110 120 130
 GAC TTC GAA GCT TTT GGT TGG GAC TGG ATC ATT GCA CCG AAA CGT
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg

 140 150 160 170 180
 TAT AGA TCC AAA CGT TAT AAA GCT AAC TAT TGC TCT GGT GAA TGC
 Tyr Arg Ser Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys

 190 200 210 220
 GAA TTC GTT TTC CTG CAG AAA TAT CCG CAT ACC CAT CTG GTT CAT
 Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His

 230 240 250 260 270
 CAG GCT AAC CCG CGT AGA TCC GCT GGT CCG TGC TGT TAT CCG ACC
 Gln Ala Asn Pro Arg Arg Ser Ala Gly Pro Cys Cys Tyr Pro Thr

 280 290 300 310
 AAA ATG TCT CCG ATC AAC ATG CTG TAT TTC AAC GGT GAA TGC CAG
 Lys MET Ser Pro Ile Asn MET Leu Tyr Phe Asn Gly Glu Cys Gln

 320 330 340 350 360
 ATC ATT TAT TGC AAA ATC CCG GCT ATG GTT GTA GAC CGT TGC GGT
 Ile Ile Tyr Cys Lys Ile Pro Ala MET Val Val Asp Arg Cys Gly

 370
 TGT TCT AGA TCT
 Cys Ser Arg Ser

FIG. 13

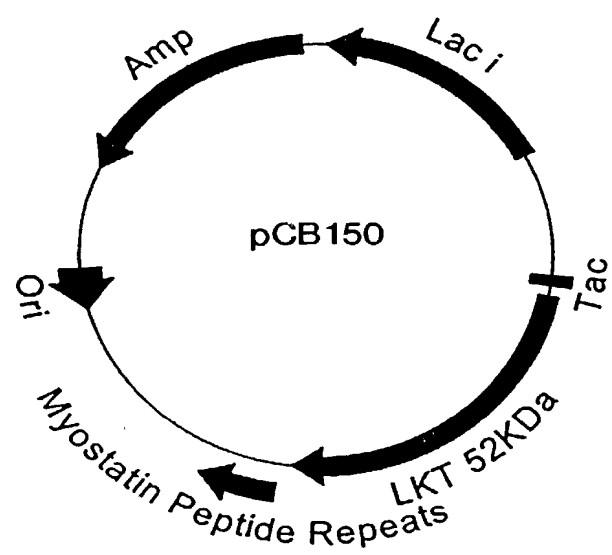


FIG. 14

3.000 3.000 3.000 3.000

1870 1880 1890 1900 1910
 ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AKA
MET Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys

1920 1930 1940 1950
 AAA ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA
 Lys Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu

1960 1970 1980 1990 2000
 CAA GGT AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG
 Gln Gly Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu

2010 2020 2030 2040
 GGG ATT GAG GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT
 Gly Ile Glu Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala

2050 2060 2070 2080 2090
 CAA ACC AGT TTA GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG
 Gln Thr Ser Leu Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu

2100 2110 2120 2130
 CGT GGC ATT GTG TTA TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG
 Arg Gly Ile Val Leu Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln

2140 2150 2160 2170 2180
 AAA ACT AAA GCA GGC CAA GCA TTA GGT TCT GCC GAA AGC ATT GTA
 Lys Thr Lys Ala Gly Gln Ala Leu Gly Ser Ala Glu Ser Ile Val

2190 2200 2210 2220
 CAA AAT GCA AAT AAA GCC AAA ACT GTA TTA TCT GGC ATT CAA TCT
 Gln Asn Ala Asn Lys Ala Lys Thr Val Leu Ser Gly Ile Gln Ser

2230 2240 2250 2260 2270
 ATT TTA GGC TCA GTA TTG GCT GGA ATG GAT TTA GAT GAG GCC TTA
 Ile Leu Gly Ser Val Leu Ala Gly MET Asp Leu Asp Glu Ala Leu

FIG. 15A

2280 2290 2300 2310
 CAG AAT AAC AGC AAC CAA CAT GCT CTT GCT AAA GCT GGC TTG GAG
 Gln Asn Asn Ser Asn Gln His Ala Leu Ala Lys Ala Gly Leu Glu

2320 2330 2340 2350 2360
 CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT AAT TCA GTA AAA ACA
 Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala Asn Ser Val Lys Thr

2370 2380 2390 2400
 CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT GGT TCA AAA CTA
 Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe Gly Ser Lys Leu

2410 2420 2430 2440 2450
 CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA CTC AAA AAT
 Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys Leu Lys Asn

2460 2470 2480 2490
 ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT ATC TCA
 Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val Ile Ser

2500 2510 2520 2530 2540
 GGG CTA TTA TCG GGC GCA ACC GCT GCA CTT GTA CTT GCA GAT AAA
 Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp Lys

2550 2560 2570 2580
 AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA
 Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala

2590 2600 2610 2620 2630
 AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT
 Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile

2640 2650 2660 2670
 TTA GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG
 Leu Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val

FIG. 15B

2680 2690 2700 2710 2720
 GCT GCT TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA
 Ala Ala Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu

 2730 2740 2750 2760
 GCA TTT GCC GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA
 Ala Phe Ala Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu

 2770 2780 2790 2800 2810
 GAG AGT TAT GCC GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT
 Glu Ser Tyr Ala Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp

 2820 2830 2840 2850
 AAT TTA TTA GCA GAA TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA
 Asn Leu Leu Ala Glu Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala

 2860 2870 2880 2890 2900
 TCG GTT ACT GCA ATT AAT ACC GCA TTG GCC GCT ATT GCT GGT GGT
 Ser Val Thr Ala Ile Asn Thr Ala Leu Ala Ala Ile Ala Gly Gly

 2910 2920 2930 2940
 GTG TCT GCT GCA GCC GAT TTA ACA TTT GAA AAA GTT AAA CAT
 Val Ser Ala Ala Ala Asp Leu Thr Phe Glu Lys Val Lys His

 2950 2960 2970 2980 2990
 AAT CTT GTC ATC ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA
 Asn Leu Val Ile Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln

 3000 3010 3020 3030
 AAC TGG TTC CGA GAG GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT
 Asn Trp Phe Arg Glu Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr

 3040 3050 3060 3070 3080
 AAA GCA ACT AAA GAT GAG AAA ATC GAA GAA ATC ATC GGT CAA AAT
 Lys Ala Thr Lys Asp Glu Lys Ile Glu Glu Ile Ile Gly Gln Asn

FIG. 15C

3090 3100 3110 3120
GGC GAG CGG ATC ACC TCA AAG CAA GTT GAT GAT CTT ATC GCA AAA
Gly Glu Arg Ile Thr Ser Lys Gln Val Asp Asp Leu Ile Ala Lys

3130 3140 3150 3160 3170
GGT AAC GGC AAA ATT ACC CAA GAT GAG CTA TCA AAA GTT GTT GAT
Gly Asn Gly Lys Ile Thr Gln Asp Glu Leu Ser Lys Val Val Asp

3180 3190 3200 3210
AAC TAT GAA TTG CTC AAA CAT AGC AAA AAT GTG ACA AAC AGC TTA
Asn Tyr Glu Leu Leu Lys His Ser Lys Asn Val Thr Asn Ser Leu

3220 3230 3240 3250 3260
GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT ACC TCG TCT AAT GAT
Asp Lys Leu Ile Ser Ser Val Ser Ala Phe Thr Ser Ser Asn Asp

3270 3280 3290 3300
TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG TTG GAT CAA AGT
Ser Arg Asn Val Leu Val Ala Pro Thr Ser MET Leu Asp Gln Ser

3310 3320 3330 3340
TTA TCT TCT CTT CAA TTT GCT AGG GGA TCC TAG
Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser ---

FIG. 15D

1 ATGCAAAAC TGCAAATCTC TGTATATT TACCTATT TA CGCTGATTGT
 51 TGCTGGCCCA GTGGATCTGA ATGAGAACAG CGAGCAGAAG GAAAATGTGG
 101 AAAAAGAGGG GCTGTGTAAT GCATGTTGT GGAGGGAAAA CACTACATCC
 151 TCAAGACTAG AAGCCATAAA AATCCAAATC CTCAGTAAAC TTCGCCTGGA
 201 AACAGCTCCT AACATCAGCA AAGATGCTAT CAGACAACTT TTGCCAAGG
 251 CTCCTCCACT CCTGGAAC TG ATTGATCAGT TCGATGTCCA GAGAGATGCC
 301 AGCAGTGACG GCTCCTTGG AGACGATGAC TACCACGCCA GGACGGAAAC
 351 GGTCAATTAC ATGCCACGG AGTCTGATCT TCTAACGCAA GTGGAAGGAA
 401 AACCCAAATG TTGCTTCTT AAATTAGCT CTAAGATACA ATACAATAAA
 451 CTAGTAAAGG CCCAACTGTG GATATATCTG AGGCCTGTCA AGACTCCTGC
 501 GACAGTGTGTT GTGCAAATCC TGAGACTCAT CAAACCCATG AAAGACGGTA
 551 CAAGGTATAC TGGAAATCCGA TCTCTGAAAC TTGACATGAA CCCAGGCACT
 601 GGTATTTGGC AGAGCATTGA TGTGAAGACA GTGTTGCAGA ACTGGCTCAA
 651 ACAACCTGAA TCCAACCTAG GCATTGAAAT CAAAGCTTTA GATGAGAATG
 701 GCCATGATCT TGCTGTAACC TTCCCAGAAC CAGGAGAAGA TGGACTGACT
 751 CCTTTTTAG AAGTCAAGGT AACAGACACA CCAAAAGAT CTAGGAGAGA
 801 TTTTGGGCTT GATTGTGATG AACACTCCAC AGAATCTCGA TGCTGTCGCT
 851 ACCCCCTCAC GGTGGATTGG GAAGCTTTG GATGGGATTG GATTATTGCA
 901 CCTAAAAGAT ATAAGGCCAA TTACTGCTCT GGAGAATGTG AATTGTATT
 951 TTTGCAAAAG TATCCTCATA CCCATCTTGT GCACCAAGCA AACCCAGAG
 1001 GTTCAGCCGG CCCCTGCTGT ACTCCTACAA AGATGTCTCC AATTAATATG
 1051 CTATATTTA ATGGCGAAGG ACAAAATAATA TACGGGAAGA TTCCAGCCAT
 1101 GGTAGTAGAT CGCTGTGGGT GCTCATGA

FIG. 16A

1 MQKLQISVYI YLFTLIVAGP VDLNENSEQK ENVEKEGLCN ACLWRENTTS
 51 SRLEAIKIQT LSCLRLETAP NISKDAIRQL LPKAPPLLEL IDQFDVQRDA
 101 SSDGSLEDD YHARTEVTIT MPTESDLLTQ VEGKPCKCF KFSSKIQYNK
 151 LVKAQLWIYL RPVKTPATVF VQILRLIKPM KDGTRYTGIR SLKLDMNPGT
 201 GIWQSIDVKT VLQNWLKQPE SNLGIEIKAL DENGHDLAVT FPEPGEDGLT
 251 PFLEVKTDT PKRSRRDFGL DCDEHSTESR CCRYPLTVDF EAFGWDWIIA
 301 PKRYKANYCS GECEFVFLQK YPHTHLVHQA NPRGSAGPCC TPTKMSPINM
 351 LYFNGEQQII YGKIPAMVVD RCGCS

FIG. 16B

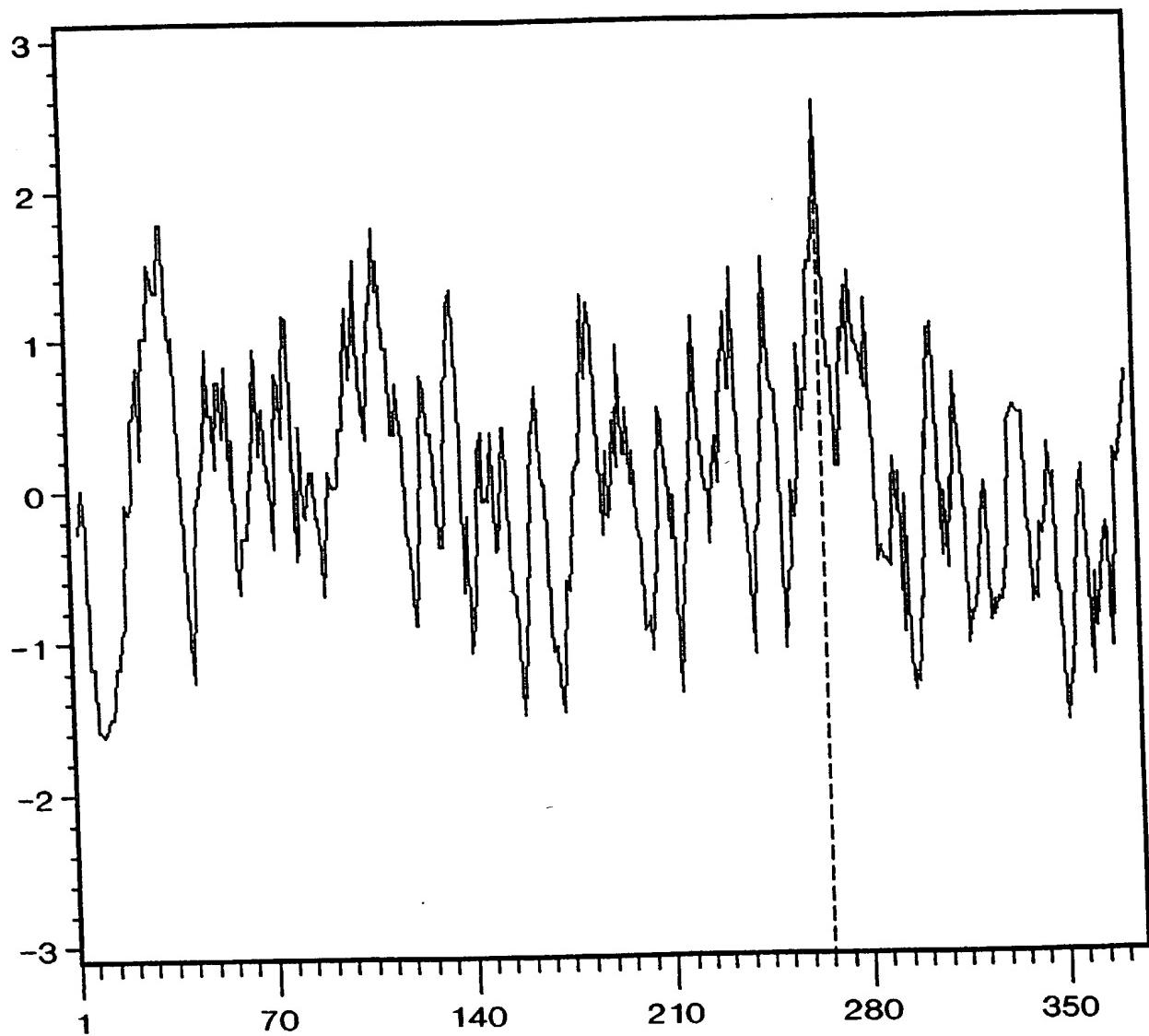


FIG. 17

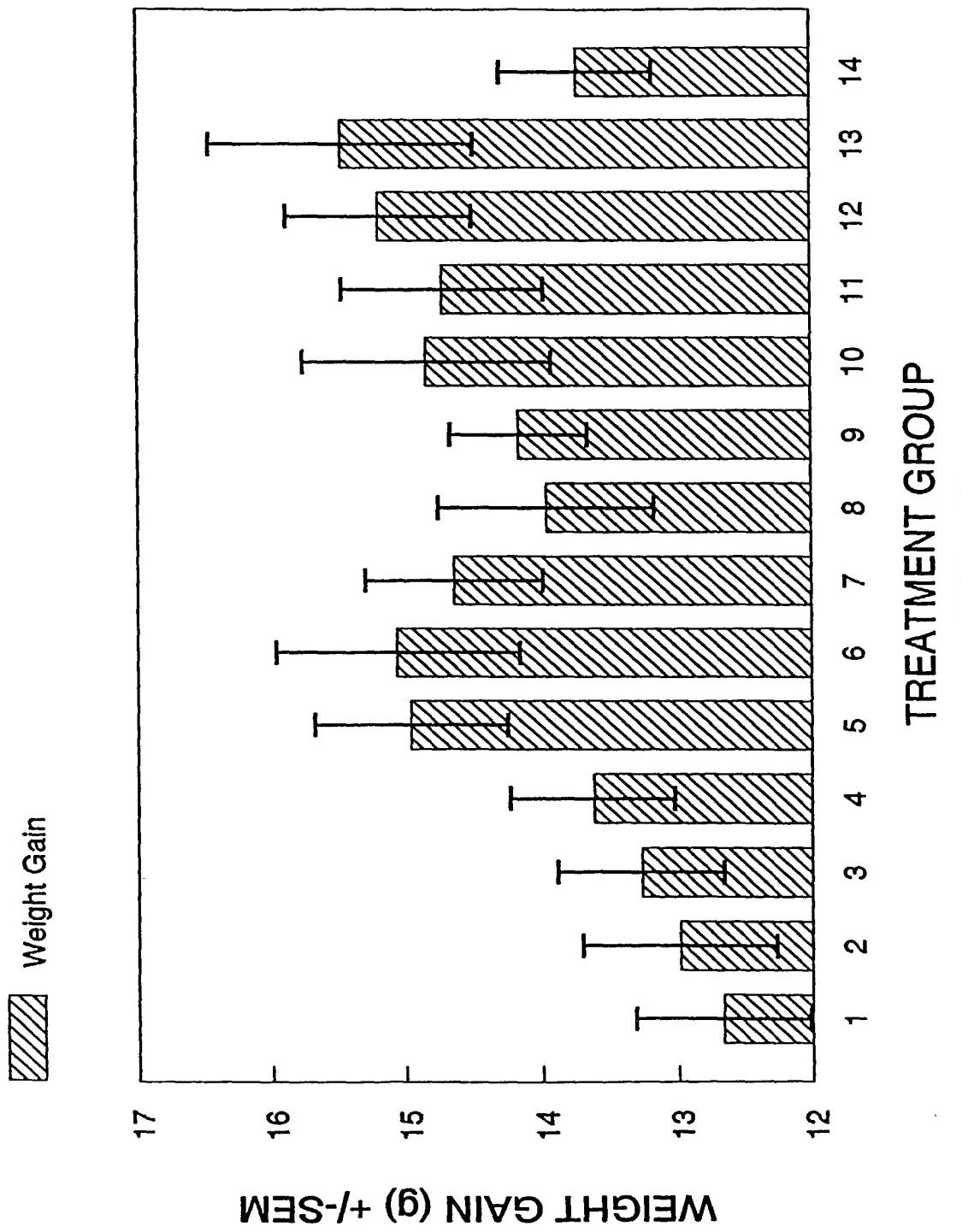


FIG. 18